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	L8	(codon near3 mammal\$) and @pd > 20031218	0
	L7	(cre recombinase) and @pd > 20031218	0
	L6	(modif\$ near3 cre recombinase) and @pd > 20031218	0
	L5	(L3 and cre) and @pd > 20030710	14
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	L3	(codon near3 mammal\$) and @pd > 20030710	69
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Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

/ol	untary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	☐ Non-Patent Literature
	(journal articles, conference proceedings, new product announcements etc.)
A	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Col	nments:

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SEARCH REQUEST-FORM

Access D8# // 1462

CRFE

Scientific and Technical Information Center

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nclude the elected species or structures, keys tility of the invention. Define any terms that nown. Please attach a copy of the cover shee	words, synonyms, acros t may have a special m	nyms, and registry numbers, and concenting. Give examples or relevant of	nbine with the concept or
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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been solit into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions rapm and rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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December 16, 2003, 00:09:53; Search time 4150 Seconds (without alignments) 10350.628 Million cell updates/sec
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Baszczynski, C.L., Lyznik, L.A., Gordon-Kamm, W.J., Guan, X., and Tagliani, L.A.
and Tagliani, L.A.
Method for the integration of foreign DNA into eukaryotic patent: US 6541231-A 5 01-APR-2003;
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llarity 100.0%; Pred. No. 4.5e-98;
Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
mol_type="genomic DNA"
[b_xref="taxon:32630"
| 383 c 339 g 124 t
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383 GCRAGGAGAACGTGGAGCGCGCCCAAGCAGGCCTTCGAGCGCACCG 362 GAAGGAAACGTGGACGCGGCGAGCGCCAAGCAGGCCTTCGAGCGCACCG 483 ACTTCGACCAGGTGCCAGTGAAACAGCAGAGCCGTCGCTTCGAGAGGCCC 422 ATTTCGACCAGGTGCCTGATGGAGAACAGCAGCTCCAGAACATCGCAACC 503 TGGCCTTCCTGGGCATCGCCTAATGAAAACAGCGCAACGCGAGACTCGCCAACC 504 TGGCGTTCCTGGGCATCGCCTAAACAACACCCTTCTGCGCAATTCGCCCGAGATCGCCGAGATCGCCGAATTCCATCGAAACAACACCTTCTGCGCAATTGCATACAACACCCTACTGCGCAATTGCCCGCATTC 563 GCGTGAAGAAATTGCATACAACACCCTCCTCAGGATCGCGGAAATTGCCCGCATTC 563 GCGTGAAGAAATTGCATACAACACCCTCCTCAGGATCGCGGAAATTGCCCGCATTC 563 GCGTGAAAGAACAACACGCTCCTCAGGATCGCGGCACCATCCTCATCAATCCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCGCATTCCTCAATCGCCCCAATTCCTCAATCGCCCGCATTCCTCAATCGCCCCAATCGCCCACCAATCGCCCAATCGCCCAATCGCCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCGCCCAATCCCAATCGCCCCCAATCCCCCCAATCCCCCCAATCCCAATCCGCCCCAATCCCCCCAATCCCCCCAATCCCCCCAATCCCCCC	DD 542 GCGTGAAGGACATTAGCCGACGGCGGCAGGATGCTTATCCACATTGGCAGGACCA 601 623 AGACCCTGGTCACCGCGGCGGCGGCGAGGATGCTTATCCACCACAGCCTGGCGCGGCGTGGCGGGGCGTGGCTGGGCGTGGCTGGGCGTGGCCTCGAGCTGGCGTGGCTGGC		Db 902 GCGCCGGTTTCCATCCCCGAAATCTTCATCATCATCATCATCATCATCATCTTCATCCCCGAACGTTG 961	AR302441

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421 437 497 541 557 601

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317 361

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661 677 721 737

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Edenhofer, F.O., Wunderlich, T. and Rajewsky, K.
Mutations of cryptic splice sites in cre and cre-fusion proteins to
improve the expression in inducibility
Patent: EP 1170344-A 7 09-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
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                258 ACCTCCTGTACCTGCAAGCCAGAGGCCTGGCTGTGAAGACCATCCAACAGACACCTGGGCC
                                                              AGCTCAACATGCTGCAGAGATCTGGCCTGCCTCGCCTTCTGACTCCAATGCTGT
                                                                                                                                                            cccrddrangagaancagaaagagagaagargragargcrddgagagagagagagagagaga
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Sequence 7 from Patent BP1170364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal sequence"

// codon start=1

// transl_table=11

/product="codon-optimized cre recombinase"

/protein_id="AAL31698.1"

/brotein_id="AAL31698.1"

/db_xref="Gal-17016300"

/translation="WYPEKREXVSNLiTVHONLPALPVDATSDEVRKNLMDMFRDRQA

FSEHTWKMLLSVCRSWAAWCKLANNRKMFRAEDEDVRDYLLYLOARGLAVKTIQQHLGQ

LNMLHERSGLEPRESDENAVSLYWRRIRKERAPDADGREELFEDPDQVRSELMBUS

DRCQDIRNLAFLGIAXUPLLAFLAEIARIRKDISRTDGGRALHIGGTERTUSGTAGUE

KALSLGVTKLVBRWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFBAT

HRLITGARDDSGQRYLAWSGGRSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMYRR
                                                            1080 bp DNA linear SYN 19-NOV-2001 construct codon-optimized cre recombinase (iCre) gene,
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14..1069
/gene="icre"
/note="contains_part of the large T nuclear localization
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                                                                                                                                                                 synthetic construct
artificial sequences.
1 (bases 1 to 1080)
Shimshek,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F.,
Stewart,F.A., Seeburg,P.H. and Sprengel,R.
Codon-Optimized Cre Recombinase Expression in the Mouse
                                                                                                                                                                                                                                                                                    2 Tobases 1 to 1080)
Shimshek, D.R., Kim, J., Huebner, M.R., Spergel, D.J., Buchholz, F.,
Stewart, F.A., Seeburg, P.H. and Sprengel, R.
Direct Submission
Submitted (13-SEP-2001) Molecular Neurobiology,
Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany
Location/Qualifiers
1. 1080
/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="derived from bacteriophage P1"
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/note="contains Kozak sequence"
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Pred. No. 2.6e-65;
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Pred. No. 8.2e-60;
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Mutations of cryptic splice sites in cre and cre-fusion proteins improve the expression in inducibility
Patent: EP 1170364-A 9 09-03N-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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028 TGCGCTC 962 CGAGGCTI AX191674 Sequence 4 AX191674 AX191674.1 Synthetic	ORGANISM synthetic construct REFERENCE artificial sequences. ATTHORS Schwenk,F. TITLE Transduction of recombinases for inducible gene targeting JOURNAL Patent: WO 0149932-A 40 12-JUL-2001, ARTEMIS Pharmaceuticals GmbH (DE) FEATURES Location/Qualifiers Source ARTEMIS Pharmaceuticals GmbH (DE) FORGINGE I. 4847 ARTEMIS Pharmaceuticals GmbH (DE) FORGINGE PATEMIS Pharmaceuticals GmbH (DE) ARTEMIS	y Match Local (GAAGGAAGGTGAGCAACCTGCTGACCGTGCACCAGAACCTGCAGAAGATTTGCAGAGACCGAGAACCTGCAAATTTGCTGACCGTACACCAAAATTTGCAGAGACCGTACACCAAAATTTGCAGAGACCTGACCGTACCCAAAATTTGCAACGAACCTGAAGATCCTGACCTGACCGAGACCTGCAACGACTTCCACCACCACGAGACCTGCAGAGACCTGACGCAGCTTTCCAGCACACTTTTCTGACCTTACCCGAAAAATTTTCTGACCTTTGCCCTTTGCCGTTGCCGCGCGTTTTCTGAACTTACCCGCAAAAATTTCTTCTCTCCCCTTTGCCGTTGCCGTTTTTTTCTGAACTACCCGAAAATTCTCTCCCGCAGAGACCTGAAGATTTCTAAAAAAAA

TITLE Conditional gene trapping construct for the disruption of genes JOURNAL Patent: WO 0129208-A 14 26-APR-2001; ARTEMIS Pharmaceuticals GMDH (DE); Frankgen Biotechnologie AG (DE) REATURES Location/Qualifiers 1. c385 /organism="synthetic construct" /mol_type="genomic DNA" /mol_type="genomic DNA" /db xref="taxon:32630" /note="vector pBABE-pgKCre" BASE COUNT 1208 a 1448 c 1402 g 1307 t	Query Match 60.9%; Score 639.4; DB 6; Length 5365; Best Local Similarity 75.6%; Pred. No. 1.3e-56; Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;	OY 1 ATGCCCAAGAAGAAGGTGAGCAACCTGCTGACGTGCACGAGAACCTGCCGGC 60	OY 61 CTGCCCGTGGACGCCACCAGCGACGAGGAAGAACCTGATGGACATGTTCCGCGAC 120	QY 121 CGCCAGGCCTTCAGCGAGCACACCTGGAAGATGCTGAGCGTGTGCCGCAGCTGGGCC 180 DD 2092 CGCCAGGCGTTTTCTGAGCATACCTGGAAATGCTTCTGTCCGTTTGCCGTCGTGGGCG 2151	QY 181 GCCTGGTGCAAGCTGAACCGCAAGTGGTTCCCCGCGAGGCCCGAGGACGTGCGCGAC 240	Qy 241 TACCTGCTGTACCTGCAGGCCCGGGCCTGAAGACCATCCAGCAGCACCTGGGC 300	OY 301 CAGGTGAACATGCTGCAGCGCAGGGCCTGCCCGGCCCAGGGACAGCAACGGTG 360	OY 361 AGCCTGGTGATGCGCGCATCCGCAAGGAAAACGTGGACGCGGCGAGCGCCAAGCAG 420 Db 2332 TCACTGGTTATGCGGCGGCGGAAAAGAAAACGTTGATGCTGAACGTGAAAAACG 2391	Qy 421 GCCCTGGCCTTCGACGACTTCGACCAGGTGCGAGCCTGATGGAGAACAGCGAC 480	Qy 481 CGCTGCCAGGACATCCGCAACCTGGCCTTCCTGGGCATCGCCTACACACCCTGCGGC 540 Db 2452 CGCTGCCAGGATATACGTAATCTGGCATTCTGGGGATTGCTTATAACACCCTGTTACGT 2511	QY 541 ATGGCCGGATCGCCGTGAAGGACATCAGCGACGACGGCGGCGCATG 600	Qy 601 CTGATCCACATCGGCCGCACCAAGACCCTGGTGAGCACCGCGGGGGAGAAGGCCCTG 660	QY 661 AGCCTGGGCGTGACCAAGCTGGAGCGCTGGATCAGCGTGAGCGGTGGCCGACGAC 720 Db 2632 AGCCTGGGGGTAACTAAACTGGTCGAGCGATGGATTTCCGTCTCTGGTGTAGATGAT 2691 QY 721 CCCAACAACTACCTGTTCTGCCGCGTGCGCAAGAACGGCGTGGCCGCCCCCAGCGCCCAC 780 Db 2692 CCGAATAACTACCTGTTTTGCCGGGTCAAAAATGGTGTTGCCGCCCCTCTGCCCACC 751	Qy 781 AGCCAGCTGAGCACCCGGGCCCTGGAGGCATCTTCGAGGCCACCCAC	
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                                                                                                                                                                                                                                                                1808 CCGGTCGATGCAACGAGTGATGAGGTTCGCAAGAACCTGATGGATTGAGGGATCGC
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                                                                                               Length 5894;
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                                                                                             Score 633.2; DB 12;
Pred. No. 5.4e-56;
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Cloning vector pTurbo-Cre
artificial sequences; vectors.

1 (bases 1 to 5894)

Lu,Z.H., Graubert,T.A. and Ley,T.J.

Direct Submission
Submitted (10-JAN-2001) Division of Oncology, Section of Stem Cell
Submitted (10-JAN-2001) Section of Stem Cell
Biology, Washington University School of Medicine, 660 South Bucild
Avenue, Campus Box 8007, St. Louis, MO 63110-1093, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MaPKKKRRVSNLLTVHQNLPALPVDATSDEVRKNLMDMFRDRQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRMLIHIGRTKTLVSTAGVE
KALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAARSATSQLSTRALEGIFEAT
HRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMNYIR
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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTWPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
                                                                                             2931
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                                                         960
GGAGCCGCGCGAGATATGGCCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT
                                                                                                                               GGCTGGACCAACGTGAACATCGTGATGAACTACATCCGCAACCTGGACAGCGAGACCGGC
                                                                                                                                                                  GGCTGGACCAATGTAATTGTCATGAACTATATCCGTAACCTGGATAGTGAAACAGG
                                                        GOCGCCCGCCGCACATGGCCCGCGCGCGTGAGCATCCCCCGAGATCATGCAGGCCGGC
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'note≈"Region: nuclear localization signal; NLS'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="rabbit beta-globin"
742. .2797
'note="contains nuclear localization signal"
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/organism="Cloning vector pTurbo-Cre"
/mol_type="cther DNA"
/db_xref="taxon:152298"
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Cloning vector pTurbo-Cre, complete sequence.
AF334827
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\transl_table=11
\product="ampicillin_resistance
                                                                                                                                                                                                      GCCATGGTGCGCCTGCTGGAGGACGGCGA 1049
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protein_id="AAK11472.1"
'db_xref="GI:12965138"
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'note="chicken beta-actin"
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complement(4885. .5745)
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TITLE
JOURNAL
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AF334827
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604 ATCCACATCCGCCGCACCAAGACCCTGGTGACCCCGCCGCGCGTGAAGGCCCTGAGC 1801 ATCCACATCGCGCGCGCGTTAGCTGCCCGCGCGCGTGAGGCCTTAGC 664 CTGGGGCGACAAACGCTGGTTAGCCCCGCGCGCGTGTGAGGCCTTAGCCCCCGCGCGGCGTGAGCGCCTTAGCCCCCCGCGCGGCGTGAGCGCCTTAGCCCCCCCGACGCCCCCCGACGCCCCCCCC	Db 2161 TGGTGGCCTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGG	RESULT 14 AX205077 LOCUS DEFINITION Sequence 7 from Patent WO0155361. ACCESSION AX205077 VERSION AX205077. VERSION AX205077.1 GI:15394318 KEYWORDS SOURCE unidentified	NISM unidentifunce unclassifunce inclassifunce incompliance Recombination Patent: Well of the Chiron Colurce	/mol_type="genomic DNA" /db_xref="texon:32644" /hoTe="recombinant DNA" BASE COUNT 1309 a 1238 c 1329 g 1385 t ORIGIN	Query Match 60.0%; Score 630; DB 6; Length 5261; Best Local Similarity 75.1%; Pred. No. 1.2e-55; Matches 786; Conservative 0; Mismatches 260; Indels 0; Gaps 0;	Qy 4 CCCAAGAAGAAGAAGGTGAGCAACCTGCTGACGTGCACCAGAACCTGCCCGCCTG 63	Qy 64 CCCGTGGACGCCACCAGGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACGC 123 Db 1261 CCGGTCGATGCAACGAGGTTCGCAAGAACCTGATGGACATTCAGGGATCGC 1320	Oy 124 CAGGCCTTCAGGAGCACACCTGGAAGATGCTGAGGGTGTGCCGCAGCTGGCCGCC 183
	for 1309 a tch al Similarity 786; Conserv	4 CCCAAGAAGAAGGAAGGTGAGCAACCTGCTGCACCAGGACCTGCCCGCCC	124 1321 184 1381 244	DD	OY 364 CTGGTGATGCGCCGCATCCGCAAGAAACGTGGACGCCGGCGAGCGCCAAGCAGCCC 423	424 C	OY 484 TGCCAGGACATCCGCAACCTGGCCTTCCTGGGCATCGCCTACAACACCCTGCTGCGCATC 543	Qy 544 GCCGAGATCGCCGCGTGAAGGACATCAGCCGCACCGCGCGCG

AUTHORS Li,Y., O'Donnell,C.P., Duan,H., Wu,Y.H. and Mcavoy,R. TITLE Methods for the controlled, automatic excision of heterologous dna from transgenic plants and dna-excising gene cassettes for use therein JOURNAL Patent: WO 0210415-A 2 07-FEB-2002; The University of Connecticut (US) FEATURES 1. 1553 Source Location/Qualifiers O'Organism="Enterobacteria phage Pl" /mol_type="genomic DNA" /db_xref="taxon:10678" BASE COUNT 424 a 340 c 394 g 395 t	Query Match 58.9%; Score 618.4; DB 6; Length 1553; Best Local Similarity 74.8%; Pred. No. 2.7e-54; Pred. No. 2.7e-54; Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0; Qy 14 AGAGGAAGGTGAGCACCGGCCGGAACCTGCCCGCCCGCCC	Qy 74 CCACCAGGACGAGGACGAGAACTGATGGACATGTTCGGGACCGCAGGCCTTCA 133	Db 657 TGANTAACGGAAATGGTTTCCCGCGGAACCTGAAGATGTTCGCGATTATCTTCTTTTTTTT	QY 374 GCCGCATCCGCAAGAAACTGGACGCCGGCCAAGCGCCCTAGGCCTTCG 433 Db 837 GGCGATCCGAAAAGAAAACTTGATGCCGGTCAAACGTCTAAACAGCTTTGG 896 QY 434 AGCGCACCGACTTCGACCAGGCGCTGATGGAAAACAGCCACCAGGACA 493 Db 897 AACGCACTGATTTCGACCAGGTTCGTTCATCGTCATGGAAAATAGCGATCGCTGCCAGGATA 956 QY 494 TCCGCAACCTGGCTTCCTCATCATCAACAACACCGCTGCGGATA 956	957 TACGTAATCTGGCATTTCTGGGGATTGCTTATAACACCCTGTTACGTATAGCCGAAATTG 101 554 CCCGCATCCGCGTGAAGGACATCACCGACCGACGGCGGCGCGCGTGATCG 613 1017 CCAGGATCAGGGTTAAAGATATCTCACGTACTGACGGGGGAGAAATGTTAATTG 107 614 GCCGCACCAAGACCCTGGTGAGCACCGCCGGCGTGAGAAGGCCCTGAGCCTGAGCGTGATTG 107	DD 1077 GCAGAACGAAAACGCTGGATTAGCACCGCAGGTGTAGCACATTAGCCTGGGGGTAA 1136 QY 674 CCAAGCTGGTGGAGCGCTGGATCGCTGAGCGCTGCCCCAACACTACC 733 1137 CTAAACTGGTCGAGCGTTGGATTCCGTCTCTCGTGTTGATCGAATAACTACC 1196 QY 734 TGTTCTGCCGCTGCGCAAGAACGGCTGGCCCCCCCAGCGCCCCCAGCTGACCACCTGATTACCGCTGATGATTACTACGACTGATGATTACTACTGCTGATTACTGCCGCCCCCCAGCCCAGCCAG
Qy 244 TGGTGCAAGTGAACAAGTGGTTCCCCGCAGAACATGAAATATTCCCGCAAAAATGTTCCCGCAAAAATGTTCCCGCAAAAATGTTTCCCGCAAAAATGTTTCCCGCAAAAATGTTTCCCGCAAAAATGTTTCCGCAAAATGTTTCCGCAAAATGTTTCCGCAAAATATT 1440 Qy 244 CTGCTGTACCTGCAGGCCCGCGGCCTGAAGACCATCCAGCACCTGGGCCAG 303 Db 1441 CTTCTATATCTTCAGGCGCGGGCGGGCGGGGGGAGTAAAAACTATCCAGCAACATTGGGCCAG 1500 Qy 304 CTGAACATGCTGCCGCGGGGGGGGGGGCCGCCCCCCCCCC	1561 CTGGTTATGCGGCGGATCCGAAAAGGTTGATGCGGTGAACGTGAAAA 124 CTGGCTTCGAGCCACCGACTTCGACCAGGTGCCGGGGAACGTGCAAAA 1621 CTGCTTCGAGCCACCGACTTCGACCAGGTGCCCAGCCTGATGGAACAGC 1621 CTGCGTTCGAACCACTGATTCCACCAGGTTCGTTCGTTCG	1681 544 1741 604	QY 664 CTGGGCGTGACCAAGCTGGAGCGTGAACGTGAGCGGCGGACGACGACCACCC 723	Db 1981 CAGCTATCAACTCGCGCCCTGGAAGGGTTTTTGAAGCAACTCATCGATTACGGC 2040	QY 964 TGGACCAACGTGAACATCGTGATGAACTACATCCGCAACCTGGACGGGGGCC 1023 Db 2161 TGGACCAATGTAAATATTGTCATGAACTATATCGTAACCTGGATAGTGAAACAGGGGCA 2220 QY 1024 ATGGTGCGCCTGCTGGAGACGGCGA 1049 Db 2221 ATGGTGCGCCTGCTGGAGAACGGCGA 1049 Db 2221 ATGGTGCGCTGCTGGAAGAACGCGA 2246	RESULT 15 AX380948 LOCUS AX380948 LOCUS BX380948 AX380948 AX380948 AX380948 AX380948 VERSION AX380948 AX380948.1 G1:19575790 KEYWORDS SOURCE ORGANISM Enterobacteria phage P1 Virises; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; P1-like viruses.

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854 ACAGCGGCCAGCGCTACCTGGCCTGGAGCGCCACAGCGCCCGCGTGGGCCCCGCCGGG 913
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                                                                            Search completed: December 16, 2003, 02:57:07 Job time : 4156 secs
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/ SIDSI / gradata/geneseq/, geneseqn.embl/NA1999.DAT:
/ SIDSI / gradata/geneseq/, geneseqn.embl/NA2000.DAT:
/ SIDSI / gradata/geneseq/, geneseqn.embl/NA2001A.DAT:
/ SIDSI / gradata/geneseq/, geneseqn.embl/NA2001B.DAT:
/ SIDSI / gradata/geneseq/, geneseqn.embl/NA2003.DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description
	1050	100.0	i	25	AAH41175	Mammalian Cre reco
10	755	71,9	2346	22		Chimeric recombina
m	754.4	71.8		22	AAD10215	Chimeric moCRE rec
4	639.4	60.9		24	AAD35273	His6-NLS-Cre-MTS f
S	639.4	6.09		22	AAD09280	pGK-cre-pA vector
9	639.4	60.9		22	AAD09269	pCMV-I-Cre-pA vect
7	639.4	60.9		24	ABT08148	Recombinase domain
00	639.4	6.09	5365	22		Retroviral vector

Recombinase domain	Plasmid pOG304M co	nant ad	Cre wild-type codi	Gene #3677 used to	P1	P1	Bacteriophage P1 s	erichia coli	DNA encoding Esche	Cre gene fragment.	Soli C	5	TAT-Cre fusion DNA	Delta VP22Cre-Stre	GST-Cre coding reg	reco	Cre recombinase-nu		Chimeric Cre-LDB-G	fusion	St			Chimeric recombina	CS vec	pCre	variant	variant	u	Escherichia coli c	Plasmid pQE30-cre,	reStrepTag f	pT7-TACS vector DN	variant	e variant	variant	
ABT08199	AAX19900		AAC62541	ABN97179	AAD35276	ABK10252	ABS57832	ABV73858	ABS76599	ABL61152	ACC44667	ABT16619	AAD09257	AAD09263	AAZ58065	ABL57498	ABL57499	ABL57500	AAV05702	AAD09259	AAD09268	AAD10216	AAD10218	AAD10219	AAD09266	AAV05703	AAC62543	AAC62545	AAC62547	AAF81258	AAS16712	AAD09267	AAD09265	\sim		254	
24	20	22	21	24	24	24	25	24	24	24	25	25	22	22	21	24	24	24	18	22	22	22	22	22	22	18	21	21	21	22	24	22	22	21	21	21	
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ALIGNMENTS

RESULT 1

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Mammalian type Cre recombinase gene modified so as to have a high expression efficiency in a mammal by selecting a codon of high frequency for use in the mammal for expressing Cre recombinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian; Cre recombinase; organ transplantation; gene therapy; animal disease model; ds.
                                                  AAH41175 standard; DNA; 1050 BP
                                                                                                                                                                                                                                                                                                                                                                       Mammalian Cre recombinase gene.
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P-PSDB; AAB98695.
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AAH41175
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GGCGCCAAGGACGACAGCGCCAGCGCTACCTGGCCTGGAGCGGCCACAGCGCCCCGCGTG
                                                      GGCGCCGCCGCGACATGGCCCGCGCGGCGTCCCCGAAATCATGCAGGCCGGC
                                                                                                                          GGCTGGACCAAGGTGAACATGGTGATGAACTACATCCGCAACCTGGACAGCGAGACCGGC
                                                                                                     GGCTGGACCAACGTGAACATCGTGAACTACATCCGCAACCTGGACAGCGAGACCGGC
                                GGCGCCGCCGCGACATGGCCCGCGCGGCGTGAGCATCCCCGAGATCATGCAGGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrating DNA of interest into genome of eukaryotic cell, by transforming plant cell with transfer cassette comprising DNA flanked by target sites for site-specific recombinases and providing recombinases in cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Site specific recombinase; expression cassette; chimeric; moCre:FLPm protein; ds.
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1..2346
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97US-0065627.
98US-0099435.
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Tagliani LA;
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Chimeric - Bacteriophage
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P-PSDB; AAE05412.
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08-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a mammalian type Cre recombinase gene. This sequence can be modified so as to have a high expression efficiency mammal by selecting a codon of high frequency for use in the mammal expressing Cre recombinase. The gene can be used in organ transplantation, gene therapy and creation of animal disease models.
                                                                                                                                                                                        DB 22; Length 1050;
                                                                                                                                                                                                                            0
                                                                                                                                                                                                                          0; Indels
                                                                                                                                                   Sequence 1050 BP; 204 A; 383 C; 339 G; 124 T; 0 other;
                                                                                                                                                                                    100.0%; Score 1050; DB 22; 100.0%; Pred. No. 2.6e-145;
                                                                                                                                                                                                                      0; Mismatches
            Page 7-9; 12pp; Japanese.
                                                                                                                                                                                                    Best Local Similarity 100.
Matches 1050; Conservative
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The invention relates to compositions and methods for introducing
a DNA of interest into a genomic target site. The methods and
compositions involve the use of a combination of target sites for two
site specific recombinases and expression of a chimeric recombinase
with dual target site specificity. The compositions comprise novel
site-specific recombinases with specificities to multiple target sites,
and mucleotide sequences and expression cassettes encoding these
and mucleotide sequences and expression cassettes encoding these
into genome of eukaryotic cell involves transforming the cell having
target sites for the novel recombinase with a DNA of interest that is
flanked by corresponding target sites. The method is useful for
constructing stably transformed eukaryotic cells, preferrably plant
cells. The present sequence is a chimeric recombinase DNA encoding
moCRE, Cre protein from Bacteriophage Pl with maize preferred codons.
                                                                                                                1021
          Maize; site specific recombinase; expression cassette; chimeric; moCRE;
                                                                                       TCATGAACTACATTGGCAACCTTGACAGGGAGGGGGGGAATGGTTCGCCTCCTGGAAG
                                                          TGATGAACTACATCCGCAACCTGGACAGCGAGACCGGCGCCATGGTGCGCCCTGCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Integrating DNA of interest into genome of eukaryotic cell, by transforming plant cell with transfer cassette comprising DNA flanked by target sites for site-specific recombinases and providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 15-16; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric moCRE recombinase DNA.
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Bacteriophage Pl.
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18-NOV-1997;
08-SEP-1998;
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constructing stably transformed eukaryotic cells, preferably plant cells. The present sequence is a chimeric recombinase DNA encoding moCre:FLPm, Cre protein from Bacteriophage Pl and FLP from Saccharomyces, both maize preferred codons.
                                                                                                                                                                                                                              0;
                                                                                                                                                                           Length 2346;
                                                                                                                                                                                                  Pred. No. 3.2e-102;
0; Mismatches 170; Indels
                                                                                                                          Sequence 2346 BP; 534 A; 807 C; 599 G; 406 T; 0 other;
                                                                                                                                                                           Score 755; DB 22;
Pred. No. 3.2e-102;
                                                                                                                                                                         71.9%;
                                                                                                                                                                                                Local Similarity 83.4 les 857; Conservative
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The invention relates to a polypeptide comprising a site-specific DNA recombinase (DRI) and a membrane translocation sequence (WTS), and nucleic acids that encode such cell-permeable recombinases. The sequences of take that encode such cell-permeable recombinases. The sequences of the invention are useful for stimulating site-specific DNA recombination in a cell and for determining the efficiency of protein transduction into a population of cells. The polypeptide of the invention is further useful for detecting whether site-specific DNA recombination has occurred within a cell and for identifying a compound that modulates unclear metabolism in a cell. It is used for identifying a peptide that behaves as a membrane translocation or nuclear localisation signal (NLS) and is also useful for identifying a compound preferably an amino acid sequence that modulates the compound preferably an acid sequence that modulates the compound activity of a polypeptide to a cell or the activity of a polypeptide to a cell or the activity of a polypeptide to a cell or the activity of a polypeptide to a cell or the activity of a polypeptide to a cell or the activity of a specific therapeutic protein, by enhancing or other activity across the blood-brain barrier. The present sequence is His6-NLS-Cre-MTS fusion DNA comprising cre gene from Bacteriophage Plana and Simian virus 40 NLS sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site-specific DNA recombinase, DR1; membrane translocation sequence; MTS; cell-permeable recombinase; nuclear localisation signal; NLS; excretion, trafficking; blood-brain barrier; His6-NLS-Cre-MTS fusion gene; chimeric; simian virus 40; SV40; gene; ds.
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/product= "His6-NLS-Cre-MTS fusion protein"
/transl_except= (pos: 1153..1155, aa:Pro-Glx)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Rhesus macaque polyoma virus.
- Bacteriophage Pl.
- Unidentified.
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Pred. No. 4.2e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA recombinase domain/protein transduction doma inducing target gene alterations in organisms or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to use of fusion proteins comprising a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is a pGK-cre-pA DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4847;
                                                                                                                                                                                                                                                                         gene alteration; fusion protein transduction domain; PTD; gene alteration; fusion protein; Human immunodeficiency virus; HIV; pGK-cre-pA vector; ds.
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         1081 GCAATGGTGCGCCTGCTGGAAGATGGCGA 1109
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                                                                                                                  BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%; Score 639.4; DB 22; Length 4960; 75.6%; Pred. No. 2.3e-85; ive 0; Mismatches 256; Indels 0;
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Best Local Similarity 75.6%;
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2000EP-0124595.
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The invention comprises the amino acid and coding sequences of fusion proteins that contain a recombinase domain and a signal peptide domain which directs nuclear import of the fusion protein in evkaryotic cells. The fusion proteins of the invention are useful for recombining the DNA molecules of cells or organisms containing recombinase recombining the DNA sequences for the recombinase domain of the fusion proteins. The fusion proteins of the invention are useful for studying gene function at various developmental stages and for the creation of transgenic organisms. The C31-Int recombination system of the invention can be used for the site-specific integration of foreign DNA into the genome of mammalian cells (e.g. for gene therapy). The present DNA sequence represents a vector that was used in the invention.
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                                                                                                TTAATCCATATTGGCAGAACGAAACGCTGGTTAGCACCACGAGTGTAGAGAAGCCACTT
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                                   CTGATCCACATCGGCCGCACCAAGACCCTGGTGAGCACCGCCGGCGTGGAGAAGGCCCTG
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GGCTGGACCAATGTAAATATTGTCATGAACTATATCCGTAACCTGGATAGTGAAACAGGG 1996
                                                    960
                                                                                                                                                                                                                                                Gene trapping construct; conditional mutation; unidirectional inversion; recombinase recognition sequence; RRS; disruption cassette; selection cassette; transgenic organism; retroviral vector; pBABA-pgkCre; cre recombinase; phosphoglycerate kinase; PGK promoter; ds.
                                                                                                                                                                                                                                 Retroviral vector pBABE-pgkCre used as gene trap in embryonic stem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product= "Bacteriophage P1 Cre recombinase protein with simian virus 40 large T-antigen N-terminal nuclear ocalisation signal"
                                GCCCCAAGGACGACAGCGCCCAGCGCTACCTGGCCTGGAGCGGCCACAGCGCCCGCGTG
                                                   GGCGCCCGCGCGCACATGGCCCGCGCGCGTGAGCATCCCCCGAGATCATGCAGGCCGGC
                                                                   GGAGCCGCGCGAGATATGGCCCCGCCGCAGTTTCAATACCGGAGATCATGCAAGCTGGT
                                                                                   GGCTGGACCAACGTGAACATCGTGATGAACTACATCCGCAACCTGGACAGCGAGACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Mouse phosphoglycerate kinase (PGK) promoter"
                                                                                                                                                                                                                                                                                                                                                               partial MMLV U3, MMLV R and MMLV U5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/note= "MMLV primer binding site and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= h
'note= "Promoter/enhancer deleted MMLV U3"
                                                                                                                                                                                                                                                                                                                                                                                                                                 DIRECT
MMLV R direct repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "3' MMLV R and MMLV U5"
                                                                                                                              GCAATGGTGCCTGCTGGAAGATGGCGA 2025
                                                                                                                     GCCATGGTGCGCCTGCTGGAGGACGCCGA 1049
                                                                                                                                                                                                                                                                                                                                                                                                 G3
                                                                                                                                                                                                                                                                                         Chimeric - Moloney murine leukemia virus.
Chimeric - Mus sp.
Chimeric - Bacteriophage Pl.
Chimeric - Rhesus macaque polyoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                partial MMLV
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= d
note= "5' MMLV US"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    packaging signal"
1417..1921
                                                                                                                                                                               AAD04928 standard; DNA; 5365
                                                                                                                                                                                                                                                                                                                                            8..480
/*tag= a
/note= "5'
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/*tag= b
/note= "5' p
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/rpt_type= ]
/note= "5' |
403..480
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The present invention relates to a conditional gene trapping construct capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by two recombinase recognition sequences (RRSs) specific to site specific recombinase which is capable of undirectional inversion of double standard DNA segment. One of the DNA segment (disruption cassette) is inserted in antisense orientation relative to the transcriptional orientation of the gene to be trapped. The other DNA segment (selection orientation of the gene to be trapped. The other DNA segment (selection cassette) is inserted in sense direction relative to the transcriptional corientation of the gene to be trapped. The coll comprising the gene corientation of the gene trapped or the identification and/or isolation of genes. The transgenic organism comprising the gene trapping construct is useful for mutationally inactivating all cellular correction at various developmental stages. The gene trapping construct is useful for mutationally inactivating all cellular genes. The present sequence is retroviral vector pBABA-pgkCre which is used as gene trap in embryonic stem (ES) cells. The vector genes to constructed by inserting Bacteriophage Pl cre recombinase coding region with a similar virus 40 large T-antigen N-terminal nuclear complexity mutine leukemia virus based vector pBABEBuro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2152 GCATGGTGCAAGTTGAATAACCGGAAATGGTTTCCCGCAGAACCTGAAGATGTTCGCGAT 2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCTGGTGCAAGCTGAACAACCGCAAGTGGTTCCCCGCCGAGGCCCGAGGACGTGCGCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New gene trapping construct capable of causing conditional mutations in genes, comprises functional DNA segment inserted in sense or antisense direction relative to gene to be trapped -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2092 GGCCAGGCGTTTTCTGAGCATACCTGGAAATGCTTCTGTCGTTTGCCGGTCGTGGGG
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larity 75.6%; Pred. No. 2.3e-85;
Conservative 0; Mismatches 256; Indels 0;
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                                                                                                       DIRECT
MMLV R direct repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ARTE-) ARTEMIS PHARM GMBH.
(FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                 /note= "3' MMLV US'
                                                               16-OCT-2000; 2000WO-EP10162.
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/partial
3187..3253
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les 793; Conserv
                                                                                                                                                                                                                                                                                                                    WO200129208-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-1999;
                                                                                                                                                                              misc feature
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                                     repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuehn R,
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The invention comprises the amino acid and coding sequences of fusion proteins that contain a recombinase domain and a signal peptide domain which directs nuclear import of the fusion protein in eukaryoric cells. The fusion proteins of the invention are useful for recombining the DNA molecules of cells or organisms containing recombinase recomplining the DNA sequences for the recombinase domain of the fusion proteins. The fusion proteins of the invention are useful for studying gene function at various developmental stages and for the creation of transgenic organisms. The C31-Int recombination system of the invention can be used for the site-specific integration of foreign DNA into the genome of mammalian cells (e.g. for gene therapy). The present DNA sequence
                                                                                                                                                                                                                                                                                Novel fusion protein useful for recombining DNA molecules in eukaryotic cells has recombinase protein which is linked to signal peptide domain which directs nuclear import of fusion protein in eukaryotic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a vector that was used in the invention.
                                                                                                                                                                                                                                                                                                                                           Example 4; Page 131-133; 150pp; English.
                                                                                                                                                                                                                                                                               Novel fusion protein useful for
                                                                                                                    10-NOV-2000; 2000EP-0124629.
17-APR-2001; 2001EP-0109543.
13-AUG-2001; 2001US-311876P.
                                                                                                                                                                                    (ARTE-) ARTEMIS PHARM GMBH.
                                                                                                                                                                                                                                              WPI; 2002-519298/55.
                                WO200238613-A2.
                                                                                       09-NOV-2001;
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                                                                       CAGCTGAACATGCTGCACCGCCGCAGCGGCCTGCCCCGCCCCAGCGACACGCCGTG
                                                                                                                                 AGCCTGGTGATGCGCCGCATCCGCAAGGAGAACGTGGACGCCGGCGAGCGCCCAAGCAG
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           TACCTGCTGTACCTGCAGGCCCGCGCCTGGCCGTGAAGACCATCCAGCAGCACCTGGGC
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                                                                                                               ATGCCCAAGAAGAAGAAGGTGAGCAACCTGCTGACCGTGCACCAGAACCTGCCCGCC
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                                                                                  Gaps
                                           Length 5878;
                                                                               °,
Sequence 5878 BP; 1259 A; 1514 C; 1756 G; 1349 T; 0 other;
                                       Score 639.4; DB 24; Length
Pred. No. 2.3e-85;
0; Mismatches 256; Indels
                                     75.6%;
                                                      Local Similarity 75.6
nes 793, Conservative
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Fusion protein; recombinase domain; signal peptide domain; gene function; nuclear import; recombinase recognition sequence; transgenic organism; C31-Int recombination system; site-specific integration; gene therapy; vector; ds.

domain-containing fusion protein-related vector 23.

(first entry)

Recombinase

ВР. 5878

DNA;

standard;

ABT08199

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  GGCTGGACCAACGTGAACATGAACTACATCGCAACTGGACAGCGAGACAGCGGGC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1937 GCCTGGACCAATGTAAATATTGTCATGAACTATATCCGTAACCTGGATAGTGAAACAGGG 1996
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                                                                                                1517 ATAGCCGAAATTGCCAGGATCAGGGTTAAAGATATCTCACGTACTGACGGGGGGAGAATG
                                                                                                                                                    1577 TTAATICCATATTGGCAGAACGAAAACGCTGGTTAGCACCGCAGGTGTAGAGAAGGCACTT
                                                                                                                                                                                AGCCTGGGCGTGACCAAGCTGGTGGAGCGCTGGATCAGCGTGAGCGGCGTGGCCGACGAC
                                             1457 CGCTGCCAGGATATACGTAATCTGGCATTTCTGGGGATTGCTTATAACACCCTGTTACGT
                                                                            ATCGCCGAGATCGCCCGCATCCGCGTGAAGGACATCAGCCGCACCGACGGCGGCCGCATG
                                                                                                                             CTGATCCACATCGGCCGCACCACAAGACCCTGGTGAGCACCGGCGGGGGGAGAAGGCCCTG
                                                                                                                                                                                                                                                                                GGCGCCAAGGACGACAGCGCCAGCGCTACCTGGCCTGGAGCGGCCACAGCGCCCGGCGTG
                          CGCTGCCAGGACATCCGCAACCTGGCCTTCCTGGGCATCGCCTACAACACCCTGCTGCGC
                                                                                                                                                                                                                               CCCAACAACTACCTGTTCTGCCGCGTGCGCAAGAACGGCGTGGCCGCCCCCAGCGCCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter; site-specific recombination; Cre recombinase; fusion gene; transgenic mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pOG304M containing mP1 promoter and Cre coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCATGGTGCGCCTGCTGGAGGACGGCGA 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997 GCAATGGTGCGCCTGCTGGAAGATGGCGA
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Mus musculus
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The present invention describes a nucleic acid construct, comprising a germline-specific promoter operably linked to a recombinase coding sequence. The construct can be useful for modulating agronomic characteristics, including (a) biotic stress tolerance, increased resistance to herbicides, pest damage, and viral, bacterial, and fungal diseases, improvement of crop nutritional quality, reduction of post-harvest losses, improved quantity and composition of endogenous properties, and production of new plant-derived compounds. The production of alleles containing single recombinase target sites and a desired mutation are useful for producing subtle and conditional mutations that require generation of alleles with minimal structural alterations. They are also useful for generating null alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing genetically lettal alleles. The recombinase constructs are expressed at high levels in the germ line, but not to a functionally significant degree in Es cells or embryonic or adult somatic tissue. This enables modulation of recombined target nucleic acid sequences in the early embryo. In addition, tissue-specific and conditional recombinatory tools permit the generation of transgenic plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animals. The present sequence represents a plasmid containing mouse protamine 1 promoter and Cre coding sequences from an example of the present invention.
        promoter
New nucleic acid construct, comprising a germline-specific operably linked to a recombinase coding sequence - useful for producing subtle, conditional or tissue-specific mutations
                                                                                                          Example 1; Page 48; 54pp; English.
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Sequence 2293 BP; 555 A; 559 C; 603 G; 576 T; 0 other;

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                                                                                        Gaps
            Length 2293;
                                                                                   0
    Score 636.4; DB 20; Length
Pred. No. 6.8e-85;
0; Mismatches 256; Indels
DB 20;
Match 60,6%;
Local Similarity 75.5%;
les 790; Conservative
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603

GCCGAGATCGCCCCCATCCGCGTGAAGGACATCAGCCGCACCGACGGCGCCGCATGCTG

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WPI; 1999-190617/16.

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TGCCAGGACATCCGCAACCTGGCCTTCCTGGGCATCGCCTACAACACCCTGCTGCGCATC
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Matches 786;
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                                                                                                                               GCCAAGGACGACAGCGCCAGCGCTACCTGGCCTGGAGCGGCCACAGAGGCCCGCGTGGGC
                                                                                                                                                                                                       delta-E1 Cre-LoxP Ad; adeno-associated virus; vector;
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/note= "SV40 polyA site"
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Rhesus macaque polyoma virus.
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/function= "loxP site"
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/note= "CMV promoter"
2251..2476
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551..1186
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Chimeric - Human cytomegal
Chimeric - Rhesus macaque
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gene therapy, ds.
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                                                                                                                                                        Producing recombinant adeno-associated virus (rAAV) vector, by stably infecting eukaryotic host cell with rAAV vectors, helper adenovirus or herpes virus, recombinant adenovirus or herpes vectors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of recombinant adenovirus delta-B1

Cre-loxP Ad, in which the B1 gene of the wild-type adenovirus is
cubstituted by plasmid DNA comprising a cytomegalovirus (CWV)
promoter inserted immediately downstream of the CWV promoter
followed by a sequence from SV40 that specifies polyadenylation mRNA, and a loxP site. The recombinant adenovirus is used as an induction system in methods of the invention. Thus, methods
and compositions are provided for producing recombinant adeno
associated virus (rAAV) vector particles by: (a) introducing into
a secondinant viral vector encoding plasmid, and (iii) a plasmid
a recombinant viral vector encoding plasmid, and (iii) a plasmid
c necoding herpesvirus, cytomegalovirus or adenoviral functions, or
a herpesvirus, cytomegalovirus or adenoviral functions, or
a herpesvirus, cytomegalovirus or adenoviral functions or
flox AAV particles and rAAV particles; and (b) introducing into a
second host cell (i) the rAAV particles or (a), (ii) a vector
that directe expression of Cre, and (ii) a vector which the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (ii) a vector with the composition of Cre, and (iii) a vector with the composition of Cre, and (iii) a vector with the composition of Cre, and (iii) a vector with the composition of Cre, and (iii) a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vectors are useful for in vivo or in vitro gene therapy and also for in vitro recombinant protein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 260; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.4e-84
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llarity 75.1%; Pred. No. 5
Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 60-62; 63pp; English.
WPI; 2001-483239/52.
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The present invention relates to the identification of recombinase wariants which have an altered specificity. They are tested using constructs containing variant recognition sites, which are not recognised by non-mutant recombinase but undergo recombination in the presence of a variant enzyme. Variant recombinases are useful in the production of genetically modified crop plants, particularly seedless varieties, and in phage packaging, which has uses in cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | GGCGCCAAGGACGACGGCCAGCGCTACTGGCCTGGAGCGCCCACAGCGCCCCGCGTG 900
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                                                                                                                                                                                                           Gaps
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                                                                                                                                                                            Length
                                                                                                                                                                                                      267; Indels
                                                                                                                                           Seguence 1172 BP; 299 A; 263 C; 323 G; 287 T; 0 other;
                                                                                                                                                                          21;
                                                                                                                                                                          DB
                                                                                                                                                                                       1e-82;
                                                                                                                                                                       Score 621.8; D
Pred. No. 1e-82
0; Mismatches
                                                                                                                                                                          59.2%;
74.5%;
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Best Local Similarity 74.5
Matches 782; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocallular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN9503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, when the commence described and diagnostic markers as well as the context of the cancer and the diagnostic markers as well as the context of the cancer and t
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printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO
                                           GGCGCCCCCCCCCATAGGCCCCCCCCGCGTGAGCATCCCCCGAGATCATGCAGGCCCGC
                                                                                      GGAGCCGCGCGGAGATATGGCCCCCGCGGAGTTTCAATACCGGAGATCATGCAAGCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%; Score 618.4; DB 24; Length 1553; 74.8%; Pred. No. 3.1e-82; tive 0; Mismatches 261; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                     GCCATGGTGCGCCTGCTGGAGGACGCGA 1049
                                                                                                                                                                                                                                                                GCAATGGTGCGCCTGCTGGAAGATGGCGA 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene #3677 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                                                                      ABN97179 standard; DNA; 1553
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1437 TAAATATTGTCATGAACTATATCCGTAACCTGGATAGTGAAACAGGGGCAATGGTGCGCC 1496
                                                                                                            TTCAGGCGCGCGCTTTAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGC 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage Pl Cre site specific recombinase gene.
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Cre; Cre/Lox; DNA excising gene cassette; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a polypeptide comprising a site-specific DNA recombinase (DR1) and a membrane translocation sequence (WTS), and nucleic acids that encode such cell-permeable recombinases. The sequences of the invention are useful for stimulating site-specific DNA recombination in a cell and for determining the efficiency of protein transduction into a population of cells. The polypeptide of the invention is further useful for detecting whether site-specific DNA recombination has occurred within a cell and for identifying a compound that modulates nuclear metabolism in a cell. It is used for identifying a peptide that behaves as a membrane translocation or nuclear localisation signal (NLS) and is also useful for identifying a compound preferably an amino acid sequence that modulates the compound preferably an amino acid sequence that modulates the compound modulates trafficking, uptake, excretion or ther activity of a specific therapeutic protein, by enhancing or other activity across the blood-brain barrier. The present sequence is Bacteriophage Pl Cre recombinase DNA.
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                                                                                                                                                                                                                                    Site-specific DNA recombinase, DR1; membrane translocation sequence, MTS; cell-permeable recombinase; nuclear localisation signal; NLS; excretion; trafficking; blood-brain barrier; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polypeptide comprising a cell-permeable site-specific DNA recombinase and membrane translocation sequence for stimulating site-specific DNA recombination in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AGAGGAAGGTGAGCAACCTGCTGACCGTGCACCAGAACCTGCCCGGCCCTGCCCGTGGACG
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                                                                                                                                                                                             Bacteriophage P1 Cre recombinase DNA.
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74.8%;
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plant where a heterologous transgene temporarily conveys a desired plant genome. This method is useful for creating a transiently transgenic plant where a heterologous transgene temporarily conveys a desired phenotypic trait to the plant. Complete or nearly complete removal of the heterologous DNA reduces the possibility of uncontrolled propagation of the transgenic species and permits crops produced from the transgenic plants. The excision of the transgenic food products from transgenic plants. The excision of the transgenic food products from transgenic plants. The excision of the transgene occurs only after the transgenic plants. The excision of the transgenes are excised from the host genome in response to a stimulus several days continued presence of transgenes could cause concern. If transgenes are excised from the host genome in response to a stimulus several days transgenes are reduced or eliminated. The progeny of the plants are also essentially free of the transgene sequences. The method helps to reduce the transgene sequences. The method helps to reduce undesirable spread of transgenes to the environment because pollen and seeds produced from transgenes to the environment because pollen and seeds produced from transgenes to the environment because pollen and seeds produced from transgenes to the environment secues pollen and seeds produced from transgenic plants are non-transgenic technology. The present sequence represents the bacteriophage PI Cre site specific recombinase gene sequence this sequence recognises the Loxy sequence. The Cre/Lox site specific secondarion while the method in the intention to each to the intention of the plants are not transgenic technology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel method for creating a transiently transgenic plant. The method comprises introducing a gene cassette containing transgenic gene sequences conferring a desirable phenotypic trait, a recombinase-type protein, sequences cleavable by a recombinase protein and a promoter to a plant. The plant is then exposed to a stimulus that activates the promoter and directs expression of the recombinase protein which excises the heterologous DNA from the plant
                                                                                                                                                                                                                                                                                                                                                                                                         Creating a transiently transgenic plant for producing non-transgenic food products, comprises introducing a gene cassette having the genome the genome.
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                          Bacteriophage Pl
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Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

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Pred. No. 3.1e-82;
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-193-503B-1
US-09-213-863-4
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Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli	6,29	000	7,2,3	28 4	76, 26, 31,
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Bassczynski, Christopher L.
APPLICANT: Bassczynski, Christopher L.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: Bukaryotic Genomes
FILE OF INVENTION: Bukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: 60/099,435
FRIOR PAPLICATION NUMBER: 60/099,435
FRIOR APPLICATION NUMBER: 60/056,627
FRIOR APPLICATION NUMBER: 60/056,627
FRIOR APPLICATION NUMBER: 60/056,633
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                                                                   Sequence 5, Application US/09193503B Patent No. 6262341
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; LOCATION: (1)..(2346)
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GENERAL INFORMATION:
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US-09-193-503B-5
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For The Integration Of Foreign DNA
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OTHER INFORMATION: Description of Artificial Sequence: sequence
OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacterlophage F
OTHER INFORMATION: ED from Saccharomyces, both maize preferred
OTHER INFORMATION: codons
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             APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6541231el Method For TITLE OF INVENTION: A No. 6541231el Method For TITLE OF INVENTION: A No. 6541231el Method For TITLE OF INVENTION: Enchange of TITLE OF INVENTION: Enchange of TITLE OF INVENTION: Enchange of TITLE OF INVENTION NUMBER: US/09/19,503 PRIOR APPLICATION NUMBER: US/09/193,503 PRIOR APPLICATION NUMBER: 60/099,435 PRIOR APPLICATION NUMBER: 60/099,435 PRIOR APPLICATION NUMBER: 60/056,627 PRIOR PILING DATE: 1998-10-18 PRIOR FILING DATE: 1997-11-18 PRIOR FILING DATE: 1997-11-18 PRIOR FILING DATE: 1997-11-18 PRIOR FILING DATE: 1997-11-18 SUPTWARE: PARCHING DATE: 2.1
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APPLICANT: Lyznik, Leszek A.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Guan, Xueni
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; Sequence 5, Application US/09415839
Patent No. 654121
; GENERAL INFORMATION:
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APPLICANT: Chiron Corporation
TITLE OF INVENTION: Recombinant AAV Packaging Systems;
FILE REPERBORE: 20263-501
CURRENT APPLICATION NUMBER: US/09/770,315
CURRENT APPLICATION NUMBER: US 60/178,536
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 4.6e-99;
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APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Eukaryotic Genomes
TITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/415,839
CURRENT APPLICATION NUMBER: US/09/193,503
FRIOR APPLICATION NUMBER: 60/099,435
FRIOR PELING DATE: 1998-11-17
FRIOR PELING DATE: 1998-11-17
FRIOR FILING DATE: 1997-11-18
FRIOR FILING DATE: 1997-11-18
FRIOR FILING DATE: 1997-11-18
FRIOR APPLICATION NUMBER: 60/065,613
FRIOR FILING DATE: 1997-11-18
FRIOR PELING DATE: 1997-11-18
FRIOR APPLICATION NUMBER: 60/065,613
FRIOR FILING DATE: 1997-11-18
FRIOR APPLICATION NUMBER: 60/065,613
FRIOR APPLICATION NUMBER: 60/065,613
FRIOR PELING DATE: 1997-11-18
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FRIOR APPLICATION NUMBER: 60/065,613
FRIOR PELING DATE: 1997-11-18
FRIOR APPLICATION NUMBER: 60/065,613
FRIOR FILING DATE: 1997-11-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                       Sequence 2, Application US/09415839
Patent No. 6541231
PENERAL INFORMATION:
APPLICANT: Baszczynski, Christopher L.
                                                                                                                                                                                                                                                                                                   APPLICANT: Lyznik, Leszek A.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Guan, Xueni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1740;
TITE OF INVENTION: Rapid Subcloning Using Site-Specific TITLE OF INVENTION: Recombination NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSEE: Medlen & Carroll. TITE OF STREET: 220 Montroll. TITE OF STREET: 220 Montroll.
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                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPRY disk
COMPUTER: PROPRY DECOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,224
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.8%; Score 617.4; DB 2; 75.1%; Pred. No. 6.1e-97; iive 0; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: BCM-02681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
COUNTRY: United Stat
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US-08-864-224-10
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Best Local 8
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Sequence 10, Application US/08864224 Patent No. 5851808 GENERAL INFORMATION: RESULT 6 US-08-864-224-10

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PEATURE:
CTHER INFORMATION: Description of Artificial Sequence:Nucleotide
CTHER INFORMATION: sequence encoding a Cre:FLPm polypeptide, Cre
CTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
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APPLICANT: Lyznik, Leszek A.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
TITLE OF INVENTION: A No. 6262341e1 Method For TITLE OF INVENTION: Bukaryotic Genomes
TITLE OF INVENTION: A NO. 626211e1
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/065,627
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
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SOFTWARE: Patentin Ve.
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LENGTH: 2346
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Db 902 GCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAAATATTG 961 Qy 983 TGATGAACTACCGCAACCTGGACACGGGGGCCCATGGTGCGCTGCTGGAGG 1042	QY 383 GCAAGGAAACGTGGACGCGAGGCGCCAAGCAGGCCCTGGACGTCGAGCGCACG 442
Db 962 TCATGAACTATATCCGTAACCTGGATAGTGAAACAGGGGCCAATGGTGCGCCTGCTGGAAG 1021	QY 443 ACTTCGACCAGGCAGCCTGATGGAGAACAGCGACGCTGCCAGGACATCGGCAACC 502
OY 1043 ACGGCA 1049	Db 422 ATTTCGACCAGGTTCGTTCACTCATGGAAAATAGCGATCGCTGCCAGGATATACGTAATC 481
701 4505514 7701 0 E 1110	482 TGGCATTTCTGGGGATTGCTTATAACACCCTGTTACGTATAGCCGAAATTGCCAGGATCA
Abs-09-19 - 503B-7; Sequence 7, Application US/09193503B; Patent No. 6262341	OY 563 GCGTGAAGGACATCAGCCGCACCGCGCGTGCTGATCCACATCGGCCGCACCA 622
; GENERAL INFORMATION: ; APPLICANT: Lyznik, Leszek A.; ; APPLICANT: Gordon-Kamm, William J.	Oy 623 AGACCCTGGTGAGCACCGCGGGGTGGAAGGCCCTGAGCCTGGGCGTGACCAAGCTGG 682
; APPLICANT: Rao, Guru, Xueni ; APPLICANT: Rao, Guru ; APPLICANT: Tagliani, Laura A. ; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into	OY 683 TGGAGCTGGATCAGCGTGAGCGGACGACGACCAACAACTACCTGTTCTGCC 742
FILE OF INVENIENCE: STAR (Amended listing) ; CURRENT APPLICATION NUMBER: US/09/193,503B ; CURRENT FILING DATE: 1998-11-17	OY 743 GCGTGCGAAGAACGGCGTGGCGCCCCCACCAGCGGCCACCAGCCGGCCC 802
60/099,43 09-08 60/056,62 11-18	Qy 803 TGGAGGGCATCTTCGAGGCCACCCGCCTGATCTACGGCGCCAAGGACGACGGCGC 862
	Qy 863 AGGGTACCTGGCCTGGAGCGCCCACGTGGCGCCGCGCGAACATGGCCC 922
; SEQ ID NO / ; LENGTH: 2346 ; TYPE: DNA ; ONGANISM: Artificial Sequence	QY 923 GCGCCGGCGTGAGCATCCCCGAGATCATGCAGGCCGGCGGCGGGCTGGACCTAGCTGAACATCG 982
; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: sequence ; OTHER INFORMATION: encoding a Cre:FLP polypeptide , Cre from ; OTHER INFORMATION: Bacteriophage Pl and FLP from Saccharomyces US-09-193-503B-7	Qy 983 TGATGAACTACATCCGCAACCTGGACACGGGGCCCATGGTGCGCCTGCTGGAGG 1042
Query Match 58.8%; Score 617.4; DB 3; Length 2346; Best Local Similarity 75.1%; Pred. No. 6.2e-97; Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;	Qy 1043 ACGCGA 1049 Db 1022 ATGCGA 1028
Oy 23 TGAGCAACCTGCTGCACCAGAACCTGCCCGCCCTGCAGAGACCACAGAG 82	RESULT 9 US-09-193-503B-8 ; Sequence B, Application US/09193503B
QY 83 ACGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACGCCTTCAGCGAGCACA 142	
Qy 143 CCTGGAAGATGCTGAGCGTGTGCCGCAGCTGGCCGCCTGGTGCAAGCTGAACACC 202	
Qy 203 GCAAGTGGTTCCCGGCGGAGGCGGGGACGTGCGGACCTGCTGCTAGCAGGCCC 262	; Illib OF INVENTION: Bakaryotic Genomes; FILE REFERENCE: 5718-66 (amended listing); FILE REFERENCE: 5718-66 (amended listing); CURRENT APPLICATION NUMBER: 18/09/193,503B
Qy 263 GCGGCCTGGCCGTGAACATCAGCAGCTGGGCCAGCTGAACATGCTGCACGCC 322	; CORKENT FILING DATE: 60/099,435 ; PRIOR FILING DATE: 1998-09-08 ; PRIOR PLING DATE: 60/056,627
OY 323 GCAGCGGCCTGCCCGCCCCAGCGAACGCCTGAGCCTGGTGATGCGCCGCATCC 382	; PRIOR FILING DAIE: 1997-11-18 ; PRIOR FILING DAIE: 1997-11-18 ; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: PatentIn Ver. 2.1

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For The Integration Of Foreign DNA
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                    TGATGAACTACATCCGCAACCTGGACAGCGAGACCGGCGCCCATGGTGCGCCCTGCTGGAGG
                                                                                                                                                                  TCATGAACTATATCCGTAACCTGGATAGTGAAACAGGGGCAATGGTGCGCCTGCTGGAAG
                                                                        GCGCCGGCGTGAGCATCCCCCGAGATCATGCAGGCCGGCGGCTGGACCAACGTGAACATCG
Gaps
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Pred. No. 6.2e-97;
0; Mismatches 256; Indels
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
ITLE OF INVENTION: Into
TITLE OF INVENTION: Into
TITLE OF INVENTION: Bukaryotic Genomes
ITLE OF INVENTION: Bukaryotic Genomes
FILE REPREBROES: 5.18-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/415,839
CURRENT FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1997-11-18
PRIOR PILING DATE: 1997-11-18
PRIOR PILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VOS: 11
SOFTWARE: PATENTIN VOY: 2.1
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APPLICANT: Lyznik, Leszek A.
APPLICANT: Gordon-Kamm, William J.
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ilarity 75.1%;
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                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OCHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
NAME/KEY: CDS
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Pred. No. 6.2e-97;
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FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/415,839
PRIOR APPLICATION NUMBER: US/09/193,503
PRIOR FILING DATE: 1998-10-12
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR PLING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baszczynski, Christopher L.
APPLICANT: Lyznik, Leszek A.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6541231e1 Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Bukaryotic Genomes
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Patent No. 6541231
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
TITLE OF INVENTION: A Into
TITLE OF INVENTION: Bukaryotic Genomes
FILE REFERENCE: 518-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/193,503
PRIOR FILING DATE: 1998-11-17
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
PRIOR PILING DATE: 1997-11-18
SPIOR RILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
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APPLICANT: Lyznik, Leszek A.
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Gordon-Kamm, William J.
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Patent No. 6541231
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Best Local Similarity 75.1%;
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US-09-415-839-8
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                                                        ACGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACCGCCAGGCCTTCAGCGAGCACA
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1089 TGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAAATATTGTCAT 1148
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849 GCGATGGATTTCCGTCTCTGGTGTAGCTGATGATCCGAATAACTACCTGTTTTGCCGGGT 908
                                                                          807 GGGCATCTTCGAGGCCACCCACCGCCTGATCTACGGCGCCAAGGACGACAGCGGCCAGCG
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                                      747 GCGCAAGAACGGCGTGGCCGCCCCCAGCGCACCAGCTGAGCACCCCGGGGCCCTGGA
                                                                                                                                                                                              CTACCTGGCCTGGAGCGGCCACAGCGCCCGCGTGGGCGCCGCCGCCGCCACATGGCCCCGCGC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08735609
Patent No. 595360
GENERALI INFORMATION:
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VEC
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TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 699 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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                                                                          APPLICANT: Greene, Amy
APPLICANT: Thode, Silke
APPLICANT: Jarnigan, Kurt
TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
TITLE OF INVENTION: Of an Integrated DNA Sequence
FILE REPERBNCE: 025.1US
CURRENT APPLICATION NUMBER: US/09/837,863
CURRENT APPLICATION NUMBER: US 60/198,498
PRIOR APPLICATION NUMBER: US 60/198,498
PRIOR APPLICATION NUMBER: US 60/198,498
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
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Pred. No. 8.6e-97;
0; Mismatches 254;
                      Sequence 23, Application US/09837863 Patent No. 6468754 GENERAL INFORMATION:
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75.2%;
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Best Local Similarity 75.2'
Matches 769; Conservative
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US-09-837-863-23
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318 Argeceaagaagaagaaggaaggreeaarriacrgaeggaacaeaaarrigeergea 377
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                                                                                                                                                                                                                                                                                                          1 ATGCCCAAGAAGAAGAAGGTGAGCAACCTGCTGACCGTGCACCAGAACCTGCCCGCC
                                                                                                                                                                          DB 2; Length 699;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                   Score 241.2; DB 2;
Pred. No. 3.8e-33;
0; Mismatches 88;
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AGCCTGGTGATGCGCCGCATCC 382
                                                                                                                                      23.0%; Scor.
77.0%; Pred
0; 1
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                                                                                                                                                                                                                                          Matches 294; Conservative
                                                                                                                                                                                                      Similarity
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                                                                                                          1 ATGCCCAAGAAGAAGAAGGTGAGCAACCTGCTGACCAGGAACCTGCCCGCC 60
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COMPUTER: 1BM PC compatible
SERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amalfitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 220 Montgomery Street, Suite 2200
              Pred. No. 3.8e-33;
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APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States Of America ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08735609
Patent No. 5994132
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AGCCTGGTGATGCGCCGCATCC 382
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TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 699 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: California
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              Best Local Similarity 77.0
Matches 294; Conservative
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US-08-735-609-11
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December 16, 2003, 02:57:14; Search time 1907 Seconds (without alignments) 1829.984 Million cell updates/sec
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1 atgcccaagaagaagaagaaa.....gcctgctggaggacggcgac 1050
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1: \cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: \cgn2_6/ptodata/2/pubpna/RCT_MBW_PUBL.seq:*
3: \cgn2_6/ptodata/2/pubpna/RCT_MBW_PUB.seq:*
4: \cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
5: \cgn2_6/ptodata/2/pubpna/US07_NBW_PUB.seq:*
6: \cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
7: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
8: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
10: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
13: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
14: \cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
15: \cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
16: \cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
16: \cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
16: \cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
17: \cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: \cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
18: \cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2201672 segs, 1661799599 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY NUC Gapoxt 1.0
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Maximum DB seq length: 2000000000
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Sequence:
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                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 3674, Ap	Sequence 8, Appli	Seguence 2, Appli	Sequence 5, Appli	Sequence 58, Appl	Seguence 3, Appli	Sequence 5, Appli	Sequence 7, Appli	Seguence 4, Appli	Sequence 7, Appli	Sequence 8, Appli
	ΔI	US-10-353-445-5	US-10-353-445-2	US-09-948-193-2	US-09-916-780A-2	US-09-880-107-3674	US-09-948-193-8	US-10-252-279-2	US-10-097-554A-5	US-10-161-403-58	US-09-853-033-3	US-09-853-033-5	US-09-853-033-7	US-10-353-445-4	US-10-353-445-7	US-10-353-445-8
		15	15	11	10	10	11	13	13	15	10	10	10	15	15	15
	Query Match Length DB	2346	1032	1158	1553	1553	1553	1553	1032	1032	1983	1983	1983	2346	2346	2346
₩	Query Match	71.9	71.8	6.09	58.9	58.9	58.9	58.9	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8
	Score	755	754.4	639.4	618.4	618.4	618.4	618.4	617.4	617.4	617.4	617.4	617.4	617.4	617.4	617.4
	Result No.		7	m	4	Ŋ	9	7	ω	0	10	11	12	13	14	15

Sequence 3, Appli	38	48	31,	4	Sequence 40, Appl	9	84,	57,	81,	59		58,	82,	26	i)	S	o,	9	4,	2	3	9	ď	4		Sequence 65, Appl		
US-10-109-812-3	US-10-353	US-10-356-088-48	US-10-	US-10-190-435-46	b	US-1	US-10-190-305A-84	US-10-190-435-57	US-10-190-305A-81	US-10-190-435-59	US-10-190-305A-83	0	US-10-190-305A-82	US-10-156-761-5612	5 US-10-156-761-1	US-09-974-300-5249	US-09-988-462-6	US-09-967-464-66	US-10-228-063-4	US-10-228-063-25	US-10-307-047-35	5 US-10-156-761-1	US-09-988-462-2	US-10-156-761-4984	US-09-205-448-7	US-09-967-464-65	US-10-241-009-57	US-10-190-434B-57
15	13 5	13	13	13	13	13	13	13	13	13	13	13	13	15	15	10	11	13	13	13	13	15	11	15	10	13	13	13
1051	2873	3034	3034	3597	3597	3231	3231	2742	2742	4713	4713	5184	5184	2394	9025608	863	3624	2568	2400	2478	2078	9025608	3468	1506	4039	2550	3261	3261
7.88.7	32.1	26.8	8.98	9.	6.6	0.6	9.0	8.9	8.9	8.7	8.7	8.7	8.7	8.5	8.5	8.4	8.4	8.3	8.3	8.3	8.3	8.3	8.2	8.5	•		8.1	8.1
ى بو	337.2	9.	81.6	104.4	104.4	95	95	93	93	91.4	91.4	91.4	91.4	88.8	88.8	88.6	88.2	87.6	87	87	86.8	86.8	86.6	98	98	85.6	85.4	85.4
16	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	c 33	34	35	36	37	38	39	40	41	42	43	44	45
															J	J												

ALIGNMENTS

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Sequence 5, Application US/10353445

Publication No. US20030119166A1

GENERAL INFORMATION:

APPLICANT: Beaccymiski, Christopher L.

APPLICANT: Beaccymiski, Christopher L.

APPLICANT: Gordon-Yamm, William J.

APPLICANT: Gordon-Yamm, William J.

APPLICANT: Rao, Guru

APPLICANT: Now INVERT: US/0030119166A1e1 Method For The Integration Of Foreign D TITLE OF INVENTION: Enkaryott Genomes

FILE REPERBNCE: 5718-66 (amended listing)

CURRENT PELLON NUMBER: US/10/333,445

CURRENT PELLON NUMBER: US/09/193,503B

PRIOR PLICATION NUMBER: (0/099,435

PRIOR PLICATION NUMBER: 60/066,627

PRIOR PLICATION NUMBER: 60/066,627

PRIOR PLICATION NUMBER: 60/066,627

PRIOR PLING DATE: 1997-11-18

PRIOR PLING DATE: 1997-11-18

SOFTWARE: PROMATION: Description of Artificial Sequence

FEATURE: NAMERORMATION: Description of Artificial Sequence

FEATURE: NORMATION: Codons

OTHER INFORMATION: Codons

COTHER INFORMATION: Codons

NAME/KEY: CDS

NAME/K
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GENERAL INFORMATION:
APPLICANT: Basaczynski, Christopher L.
APPLICANT: Lyznik, Leszek A.
APPLICANT: Gardon-Kamm, William J.
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Wowner
TITLE OF INVENTION: Bukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/09/193,503B
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR PILING DATE: 1997-11-18
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                                                                                                                                                                      Sequence 2, Application US/1035. Publication No. US20030119166A1 GENERAL INFORMATION:
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Qy 443 ACTTCGACCAGGTGCCAGCCTGATGGAACAGCGACCGCTGCCAGGACATCCGCAACC 502 Db 422 ATTTCGACCAGGTCGCAGGCTGATGGAACAGCGACCAGGACATTAGGAAC 481 Qy 503 TGGCCTTCCTGGGCCTCACAACACCCTGCTGCGCGATCGCCGGATTC 562 Db 482 TGGCGTTCCTCGGAATTGCATACAACACCCTCCTCAGGATCGCCGGATTC 541 Qy 563 GCGTTCCTCGGAATTGCATACAACACGCGCGCTCCTCAGGATCGCCGGAATTGCCGCACTC 541 Qy 563 GCGTGAAGGACATTGCATACCACGACGGGGCGCTGCTGATCGCCGCACCA 622 Db 542 GCGTGAAGGACATTAGCCGCACCGACGGCGCACGCACCACATTGGCAGGACCA 622 Db 542 GCGTGAAGGACATTAGCCACCGACGGCGCACGCACCAACACTTATCCACATTGGCAGGACCA 601	QY 623 AGACCCTGGTGACCGCCGGCGTGGAGGAGGCCCTGGGCGTGACCAGGTGG 682	Qy 683 TGGAGCGTGGATCAGCGTGGCCGACGACCCCAACAACTACCTGTTCTGCC 742 Db 662 TCGAACGCTGGATCTCCGGCGTCGCGGACGACCAACCAAC	Oy 743 GCGTGCGCAAGAACGGCGTCCCCAGCGCCCAGCCAGCCAG	QY 803 TGGAGGGATCTTCGAGGCCACCCACCGCCTGATCTACGGCGCCAAGGACGACGACGGCGCC 862	QY 863 AGCGCTACCTGGAGCGGCCACAGGCCCGCGTGGGCGCCGCGCGCACATGGCC 922 Db 842 AACGCTACCTCGCATGGTCCGGGCACATGGCCCGCGTTGGAGCTGCTAGGACATGGCC 901	QY 923 GCGCGGGCGTGAGCATCCCCGAGATCATGCAGGCGGCGGCTGGACCAACGTGAACATCG 982 	QY 983 TGATGAACTACATCCGCAACTGGACAGCGAGCGCGCCATGGTGCGCCTGCTGGAGG 1042	Oy 1043 ACGCGAC 1050 Db 1022 ATGGTGAC 1029	RESULT 3 193-2 - Samaiana 2 Amliation He/hoodeles	Sequence 2, approximation 03/03/35A1 ; General information: ; APPLICANT: Riley, H. Earl ; APPLICANT: Riley, H. Earl	TITLE OF	COURRENT AFFILATION NUMBER: US/US/948, L93 ; CURRENT FILING DATE: 2001-09-07 ; PRIOR APPLICATION NUMBER: 60/230, 690 ; PRIOR FILING DATE: 2000-09-07	NOTION SEQ ID NOS: 21 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 IENGTH: 1158) ORGANISM Artificial Sequence ; PEATURE: ; OTHER INFORMATION: Description: His6-NLS-Cre-MTS	Ouery Matches

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1137 CTAAACTGGTCGAGCGATGGATTTCCGTCTCTGGTGTAGCTGATGATCCGAATAACTACC 1196
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58.9%; Score 618.4; DB 10;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261;
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APPLICANT: Wockley, Joseph G.
APPLICANT: Scheff, Uwe
APPLICANT: Scheff, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-25028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3674
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                                                     Sequence 2, Application US/09916780A

Sequence 2, Application US/09916780A

Sequence 2, Application US/09916780A

GENERAL INFORMATION:

APPLICANT: University of Connecticut

APPLICANT: University of Connecticut

TITLE OF INVENTION: Methods for the Controlled, Automatic Excision of Heter

TITLE OF INVENTION: Trangenic Plants and DNA-Excising Gene Cassettes for I

FILE REFERENCE: 883933.0066

CURRENT APPLICATION NUMBER: US/09/916,780A

CURRENT FILING DATE: 2001-07-27

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.0

SEQ ID NOS: 11

SEQ ID NOS: 11
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Pred. No. 5.1e-127;
0; Mismatches 261;
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                                                                                                                                                        Length 1553
                                                                                                    gene encoding Cre recombinase
                                                                                                                                                    Score 618.4; DB 11; Length
Pred. No. 5.1e-127;
0; Mismatches 261; Indels
FastSEQ for Windows Version 4.0
                                                                                                CTHER INFORMATION: Description:
US-09-948-193-8
                                                                                                                                                    Query Match 58.9%;
Best Local Similarity 74.8%;
Matches 775; Conservative
                                                TYPE: DNA ORGANISM: Bacteriophage
                                   LENGTH: 1553
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SOFTWARE: SEQ ID NO 8
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                                       TTCAGGCGCGCGCGCTCTGGCAGTAAAAACTATCCAGCAACATTTGGGCCCAGCTAAAACATGC
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                TGCAGGCCCGCGCCCTGGCCGTGAAGACCATCCAGCAGCACCTGGGCCCAGCTGAACATGC
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US-09-948-193-8

US-09-948-193-8

Sequence 8, Application US/09948193

Publication No. US20030027335A1

GENERAL INFORMATION:

APPLICANT: Ruley, H. Earl

APPLICANT: To', Deawoong

TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA

TITLE OF INVENTION: Site-Specific Recombinases

FILE REFERENCE: 22000.0109U2

CURRENT APPLICATION NUMBER: US/09/948,193

CURRENT FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 60/230,690

PRIOR FILING DATE: 2000-09-07

NUMBER OF SEQ ID NOS: 21
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Sequence 5, Application US/10097554A

Publication No. US20030170642A1

GENERAL INFORMATION:

APPLICANT: Jeremy Scot Caldwell

APPLICANT: Jeremy Scot Caldwell

APPLICANT: Mikunj V. Somia

APPLICANT: Nikunj V. Somia

APPLICANT: Michael P. Cooke

APPLICANT: Michael P. Cooke

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APPLICANT: With Michael P. Cooke

FILE REFERENCE: 30417-1312

CURRENT FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                            CCCGCATCCGCGTGAAGGACATCAGCCGCACGGACGGCGGCGCATGCTGATCCACATCG
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CTHER INFORMATION: nucleotide sequence encoding Cre recombinase US-10-097-554A-5
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Sequence 2, Application US/10252279
Publication No. US20030190746A1
GENERAL INFORMATION:
APPLICANT: Xiao Xiao
APPLICANT: Xiao, Xiao
TITLE OF INVENTION: CELL LINES
FILE REFERENCE: 020059
CURRENT APPLICATION NUMBER: US/10/252,279
CURRENT APPLICATION NUMBER: 60/369,987
PRIOR APPLICATION NUMBER: 60/369,987
PRIOR APPLICATION NUMBER: 60/369,987
SEQID NOS: 7
SOFTWARE: Patentin version 3.1
SEQID NO 2.7
                                                                                                                                                       477 AGTGTTAAATGTCCAATTTACTGACCGTACACCAAAATTTGCCTGCATTACCGGTCGATG 536
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Pred. No. 5.1e-127;
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CTHER INFORMATION: nucleotide sequence encoding Cre recombinase US-10-161-403-58
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Pred. No. 8.6e-127;
0; Mismatches 256;
                                                                            GENERAL INFORMATION:
APPLICANT: Perez. Carl
APPLICANT: Perez. Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: 00/294, 758
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-05-31
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SRIOR APPLICATION NUMBER: 60/366, 891
PRIOR FILING DATE: 2002-05-31
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Best Local Similarity 75.1%;
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OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence OTHER INFORMATION: Homosapiens-Bacteriophage Pl
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Patent No. US20020100068A1
GENERAL INFORMATION:
APPLICANT: CHAMBON, PIERRE
APPLICANT: CHAMBON, PIERRE
TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
TITLE OF INVENTION: MEDICATED BY MODIFIED CRE-ER
FILE REFERENCE: 065691/0222
CURRENT APPLICATION NUMBER: US/09/853,033
CURRENT FILING DATE: 2000-105-11
PRIOR APPLICATION NUMBER: FR 00/12570
PRIOR PLING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 8.3e-127;
0; Mismatches 256; Indels 0;
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Patent No. US2002010068A1
GENERAL INFORMATION:
APPLICANT: CHAMBOTON:
TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
TITLE OF INVENTION: MEDITED BY MODIFIED CRE-ER
FILE REFERENCE: 065691/022
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: FR 00/12570
PRIOR PELICATION NUMBER: FR 00/12570
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: Description of Artificial;
OTHER INFORMATION: Homosapiens-Bacteriophage
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ORGANISM: Artificial sequence
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JOHER INFORMATION: Description of Artificial Sequence: Chimeric sequence : OTHER INFORMATION: Homosapiens-Bacteriophage Pl
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                                TARGETED RECOMBINATION
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Pred. No. 8.3e-127;
0; Mismatches 256; Indels
APPLICANT: METZGER, DANIEL

TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RI
TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
FILE REFERENCE: 065691/0222
CURRENT APPLICATION NUMBER: US/09/853,033
CURRENT FILING DATE: 2001-05-11
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 75.1%;
Matches 771; Conservative
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NAME/KEY: CDS
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PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 771; Conservative
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OTHER INFORMATION:
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Publication No US20030119166A1
GENERAL INFORMATION:
APPLICANT: Lyznik, Leszek A.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. US20030119166A1e1 Method For TITLE OF INVENTION: BUAALYOTIC Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION UNBER: US/10/353,445
CURRENT APPLICATION NUMBER: US/09/193,503B
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APPLICANT: BASZCZYNSKİ, Christopher; APPLICANT: Gordon-Kamm, William J.; APPLICANT: Gordon-Kamm, William J.; APPLICANT: Guan, Xueni
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APPLICANT: Baszczynski, Christopher L.
APPLICANT: Baszczynski, Christopher L.
APPLICANT: Baszczynski, Christopher L.
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Goal Genomes
TITLE OF INVENTION: A No. US20030119166Alel Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Bukaryotic Genomes
FILE REFERENCE: 5718-66 (anended listing)
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/10/353,445
CURRENT FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR PELING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SCHYMARE: Patentin Ver. 2.1
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Publication No. US20030119166A1
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ORGANISM: Artificial Sequence
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                                                                                                              AAACGCTGGTTAGCACCGCAGGTGTAGAGAAGGCACTTAGCCTGGGGGTAACTAGG
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                                                                          AGACCCTGGTGAGCACCGCCGGCGTGGAGAAGGCCCTGAGCCTGGGCGTGACCAAGCTGG
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APPLICANT: Rao, Guru

APPLICANT: Tagliani, Laura A.

TITLE OF INVENTION: A No. US20030119166Alel Method For The Integration Of Foreign DNA

TITLE OF INVENTION: Bukaryotic Genomes

TITLE OF INVENTION: Bukaryotic Genomes

FILE REFERENCE: 5718-66 (amended listing)

CURRENT PAPLICATION NUMBER: US/09/193,503B

PRIOR FILING DATE: 1908-11-17

PRIOR APPLICATION NUMBER: US/09/193,503B

PRIOR FILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-11-18

PRIOR FILING DATE: 1997-11-18

PRIOR FILING DATE: 1997-11-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PALCHIN VOR: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 617.4; DB 15; Length 2346;
Pred. No. 8.2e-127;
0; Mismatches 256; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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75.1%;
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Best Local Similarity 75.13
Matches 771; Conservative
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                         nucleic search, using sw model
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Maximum DB
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Database

AW211972 uo79f01.x AW211972 uo79f01.x AW210918 uo89609, y BI556329 6032037449 CC405275 PUHAX22TD BZ728954 CGEDN92TM ALO04689 F. TUDTIPE ALO53013 Drosophil BG483660 WHEB511 B BH29474 HVSME1001 BE564057 pacs2-164 AL223901 Tetracodon BC564057 pacs2-164 AL223901 Tetracodon BC564057 pacs2-164 AX103647 Zea mays CD645203 CSANED054 CB642003 CSANED065 CB642003 CSANED065 CB623105 CSINED065 CB623105 CSINED15A CB650537 OSANED15A CB650537 OSANED15A CB650537 OSANED15A CB650537 OSANED15A CB650537 OSANED15A CB650537 OSANED15A CB650505 OSINED105 CB653003 OSSINED105 CB653003 OSSINED107 CB653003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB623003 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107 CB622063 OSSINED107

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NOTITNI	buszyszski nci_cgar_mams mus musculus cDNA clone IMAGE:5338806 5',
	mRNA sequence.
CESSION	B1651236
RSION	BI651236.1 GI:15565472
YWORDS	BST.
URCE	Mus musculus (house mouse)
ORGANISM N	Mus musculus
#4	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi:
_	Mammalia, Butheria, Rodentia, Sciuroquathi, Muridae, Murinae, Mus
FERENCE 1	1 (bases 1 to 688)
AUTHORS N	NIH-MGC http://mgc.nci.nih.gov/.
TITLE N	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL L	Unpublished
MMENT	Contact: Robert Strausberg, Ph.D.
щ	Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: Lothar Henniquansen Ph.D., Chu-Xia Dang Ph.D.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
#	found through the I.M.A.G.E. Consortium/LLNL at:
نحد	http://image.llnl.gov
щ	Plate: LLAM11860 row: h column: 07
ц	High quality sequence stop: 688.

BI651236 603298328 AW211323 uo79f01.y B1650191 603296283 AW212478 uo89c09.x

BI651236 AW211323 BI650191 AW212478

2676

688 431 563 340

37.1 22.0 17.3 15.1

390 231 181.2 158.8

DB

Query Match Length

Score

Result No.

Description

SUMMARIES

ALIGNMENTS

CB622964 CB669047

BZ532691 CB622999

CB625663

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                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 431)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                       Thunor dene Index
Unpublished
Other_ESTS: uc79f01.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can I
found through the I.M.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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       to SW:RECR_BPP1 P06956 RECOMBINASE CRE. [1]
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High quality sequence stop: 279.
Location/Qualifiers
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                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                          GI:6517271
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                                                                            AW211323.1
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ORIGIN
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Matches
                                                                                                                                                                                                                                   AUTHORS
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                                                    ACCESSION
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Pred. No. 4
Location/Qualifiers
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Best Local Similarity 74.8%;
Matches 489; Conservative
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/d_ne="IMAGE:2649172"
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/tissue_type="tumor, gross tissue"
/dev stage="tol" months"
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/note="forgan: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
86 t
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Email: Gapbs-rémail.nih.gov

Tissue Procurement. Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                       AW212478

340 bp mRNA linear EST 03-DEC-1999 uo89c09.xl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:2649712 3' similar to SW:RECR_BPP1 P06956 RECOMBINASE CRE. [1] ;, mRNA
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                                                   CCCGAGATCATGCAGGCCGGCGGCTGGACCACGTGAACATCGTGATGAACTACATCCGC 999
                                                                                            181 CCGGAGATCATGCAAGCTGGTGGTCCTATGTAAATATTGTCATGAACTATATCCGT 240
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  121 TCTGGACACAGTGCCCGTGTCGGAGCCGCGCGAGATATGGCCCGCGCGCTGGAGTTTCAATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 340)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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larity 76.0%; Pred. No. 7.2e-19;
Conservative 0; Mismatches 62; Indels 0
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High quality sequence stop: 158.
Location/Qualifiers
1. .340
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AW212478.1 GI:6518565
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Site 2: Not1; Cloned unidirectionally. Primer: Gligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
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                                                                                                                                                                                                                                                                                                                                           BI650191 563 bp mRNA linear EST 12-SEP-2001
GTAATCTGGCATTTCTGGGGATTTGCTTATAACACCCGGTACCTATAGCCCGAAATGCCA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGCCGCCCCCAGCCACCAGCCAGCTGAGCACCCGGGCCCTGGAGGGCATCTTCGAG 819
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                                                                             919
                                                                                                    361 GGATCAGGGTAAAAGATATCTCACGGTCTGACGGGGGGGAAATGGTAATCCATATTGGGA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 53.
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11855 row: f column: 22
                                                                          GCATCCGCGTGAAGGACATCAGCCGCACCGACGGCGGCGCATGCTGATCCACATCGGCC
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Pred. No. 7.7e-23;
0; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="129.C57BL/6J,FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5336B53"
/tissue type="tumor, gross tissue"
/dev stage="10 months"
/lab_host="DH10B"
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Location/Qualifiers
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Mus musculus
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133 c 149
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Best Local Similarity 76.6%;
Matches 222; Conservative (
                                                                                                                                                                       617 GCACCAAGACC 627
                                                                                                                                                                                                                  GAAGCGAAACC 431
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TITLE
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BI650191
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292 ACTCGCGCCCTGGAAGGGAT-TTCTAAGCCACTCGATTGATTTACGGCGCTAAGGAT 234
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Unpublished
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AW210918
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ORIGIN
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                                                                                                                                                                                                                                                                                                                      AW211972 338 bp mRNA linear EST 03-DEC-1999 uc79f01.x1 NCI_CGAP_Mam3 Mus musculus cDNA clone INAGE:2648761 3' similar to SW:RECR_BPP1 P06956 RECOMBINASE CRE. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other ESTS: uo79f01.yl

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                              CGTGAACATCGTGATGAACTACATCCGCAACCTGGACAGCGAGACCGGCCCATGGTGCG 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally, Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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                                                                               114
TGATTCTGGTCAGAGATACCTGGCCTGGTCTGGACACAGTGCCCGTGTCGGAGCCGCGCG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 338) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                        54
                                                                       173 AGATATGGCCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAA
                                     CGACATGGCCCGCGCGCGTGAGCATCCCCGAGATCATGCAGGCCGGCGGCTGGACCAA
                                                                                                                                                  113 TGTAAATATTGTCATGAACTATATCCGTAACCTGGATAGTGAAACAGGGGCAATGGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="129.C57BL/6J,FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:2648761"
/tissue type="tumor, gross tissue"
/dev stage="tumor, gross tissue"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 150.6; DB 9;
Pred. No. 2.1e-17;
0; Mismatches 59;
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -40UP from Gibco
High quality sequence stop: 151.
Location/Qualifiers
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                                                                                                                                                                                        CCTGCTGGAGGACGGCGA 1049
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76.7%;
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Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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ORIGIN
                                                                                                                                                                                                                                                                                   RESULT 5
AW211972/c
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/organism="Mus musculus"
/mol type="mRNA"
/mol type="mRNA"
/strain="129.57BL/6J.FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:2649712"
/tissue type="tumor, gross tissue"
/dev stage="10 months"
/dev stage="10 months"
/downer="mage": your constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
// cothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Straubberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                    1032
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343 bp mRNA linear EST 03-DEC-1999 uo89c09.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:2649712 5' similar to SW:RECR_EP1 P06956 RECOMBINASE CRE. [1] ;, mRNA
                                173 CATATGGCCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAAT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus musculus
Mumalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 343)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                             113 GTAAATATTGTCATGAACTATATCCGTAACCTGGATAGTGAAACAGGGGCAATGGTGCGC
913 GACATGGCCCGCGCCGCGCGTGAGCATCCCCGAGATCATGCAGGCCGGCGGCGGCTGGACCAAC
                                                                                                                                                                                                                                          GTGAACATCGTGATGAACTACATCCGCAACCTGGACAGCGAGACCGGCGCCCATGGTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 128.2; DB 9 Pred. No. 2.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stop: 222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40RP from Gibco
High quality sequence stop: 2
Location/Qualifiers
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66.5%;
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Best Local Similarity
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279

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CC405275 822 bp DNA linear GSS 19-MAY-2003 PUHJX22TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa468C20,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                    916 ATGCCCGCCCGCCGTGAGCATCCCCGAGATCATGCAGGCCGGCGGCTGGACCAACGTG
                                                                                                                                                                                                                                                                                                   220 AATAITGICATGAACTATATCCGTAACCTGGATAGTGAAACAGGGGCAATGGTCCGCCTG
                                                                                                                                                                                                                                                                976 AACATCGTGATGAACTACATCCGCAACCTGGACAGCGAGACCGGCGCCCATGGTGCGCCTG
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                                              Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
                                                                                                   30; Indels
                                        Score 86; DB 12;
Pred. No. 7.4e-06;
                                                                                                0; Mismatches
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/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence
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                                        8.2%;
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Other_GSSs: PUHJX22TB
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                                     Query Match
Best Local Similarity 77.6
Matches 104; Conservative
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/note="Organ: māmmary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
        a;
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                                                                378
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                       319 CGCCGCAGCGGCCTGCCCCCCCCAGCGACAGCAACGCCGTGAGCCTGGTGATGCGCCGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Henighausen Ph.D., Chu-Xia Deng
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAMI134 row: p column: 12
        5,
     Mismatches 110; Indels
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/strain="129.C57BL/6J,FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5290619"
/tissue type="fumor, gross tissue"
/dev stage="10 months"
/lab_host="DH100"
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Location/Qualifiers
1. 836
/organism="Mus musculus"
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  Conservative
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288 bp DNA linear GSS 18-SEP-1997 clone 122014bG11, genomic survey sequence.
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Takifugu rubripes
Takifugu rubripes
Takifugu rubripes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
Blgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Direct Submission
                                                                                                        CGACTICGACCAGGIGCGCAGCCIGAIGGAGAACAGCGACCGCIGCCAGGACAICCGCAA 500
644 CAGCACCAACAACGIGGGCCACTICCAGCTCGIGCTCACGGCCATCGGCAACTTCTGCAI 585
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clade, Panicoideae, Andropogoneae, Zea.
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/db xref="taxon:4577"
/db xref="taxon:4577"
/clone="xmmawa0251P16"
/clone=lib="xm 0.7 1.5 KB"
/note="Vector: pBGK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., *A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., *R., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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9712 Medical Center Drive, Rockville, MD 20850,
TEL: 301-838-0208
Fax: 301-838-0208
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Similarity 46.9%; Pred. No. 4.2e-05;
94; Conservative 0; Mismatches 327;
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/strain="B73"
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/organism="Zea mays"
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/wolltivar="Chinese Spring"
/wolltivar="Chinese Spring"
/db xxf="reaxon:4565"
/clone="WHE3511 Boo D1"
/tissue_type="Roots"
/dev stage="Rul tillering"
/dev stage="Rul tillering"
/dev stage="Rul tillering"
/dev stage="Rul tillering"
/lab_host="E. coli Solk"
/lab_host="E. coli Solk"
/note="Wector: Lambda Uni-ZAP XR, excised phagemid
/note="Wector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(+); Site= 1: EcoRI; Site= 2: khof; Plants
were grown until full tillering stage and root tissue was
collected at Texas Tech Univeristy (Zhang, HT Nguyen Lab
). Total RNA and poly(A) RNA were prepared, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript SK(+) phagemids in the TJ
close lab (Close, Fenton) at the University of California
, Riverside. Colony plating, plasmid DNA preparations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ483660 727 bp mRNA linear EST 03-JUN-2002 WHE3511_B06_D11ZS Wheat unstressed root cDNA library Triticum aestivum cDNA clone WHE3511_B06_D11, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
         1 (bases, toronto).
Anderson,O.D., Chao,S., Close,T.J., Crossman,C., Fenton,R.D., Laz, G.R., Nguyen,H.T., Rausch,C.J., Wilson,C., Woo,J. and Zhang,D. The structure and function of the expressed portion of the wheat Unstressed root cDNA library
                                                                                                                                                                           CCTGTTCTGCCGCGCGCGAAGAACGGCGTGGCCGCCCCCCAGCCACCAGCTGAG
                                                                                                                                                                                                                                                                                               852 CGACAGCGGCCAGCGCTACCTGGACCGGCCACAGGCGCCCGCGTGGGCGCCCCC
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                                                                                 GACCAAGCTGGTGGAGCGCTGGATCAGCGTGAGCGGCGTGGCCGACGACCAACAACTA
                                                                                                              CACCCGGGCCCTGGAGGGCATCTTCGAGGCCACCCACCGCCTGATCTACGGCGCCCAAGGA
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    .727
    /organism="Triticum aestivum"

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Triticum aestivum
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Location/Qualifiers
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BQ483660.1 GI:21319596
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US Department of Agricu
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Fax: 5105595818
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Web: www.genoscope.ons.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Bark-ley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffallo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's land by and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSO091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                    113
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Moptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                        Score 79.8; DB 29; Length 288; Pred. No. 8.5e-05; O; Mismatches 22; Indels 0
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
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(all other authors)."
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/note="Wetcor: pBluescript SK(-); Site 1: EcoRI; Site_2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muchlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Reinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) CDNA phagemids (Choi, Fenton, Malarrasi)
. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Ming). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
envisors.
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http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ. Wing R, Kleinhofs A, Wiss R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
311 c 3 others
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/clone_lib="Hordeum vulgare spike EST library HVcDNA0012
(Fusarium infected)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Hordeum vulgare subsp. vulgare"
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                                                                                                                            SC 29634, USA
Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 4298
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 560
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High quality sequence stop: 735.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:112509"
/clone="HVSME10015024f"
/tissue_type="Spike"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="Morex"
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sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
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Pred. No. 0.00087
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Spencer, D.H., Raymond, C.K., Smith, E.E.,
Burns, J.L., Kaul, R. and Olsen, M.V.
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J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
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// Organism=="RDDGcenum voltgare sousp. vorgate
// Cullivar="CI16155 (Mla13)"
// Cullivar="CI16155 (Mla13)"
// Lissue type="seedling green leaf"
// Lissue type="seedling green leaf"
// Lissue type="seedling green leaf"
// Lissue type="seedling green leaf"
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// Lissue type="seedling green leaf"
// Lobe="Wector: lambdaZAP; Site=1: EcoR1; Site=2: Xho1;
// Lote="Wector: lambdaZAP; Site=2: Xho1;
// Lote="Wector: lambdaZAP; Site=1: EcoR1; Site=2: Xho1;
// Lote="Wector: lambdaZAP; Site=1: EcoR1; Site=2: Xho1;
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// Lote="Wector: lambdaZAP; Site=2: Xho1;
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// Lote="Wector: lambdaZAP; Site=2: X
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantaa; Ereptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                  998
                                                                                                                                                              417 GCTGGCCAACGTCTACCTCGCGTACCGTGACAACCCCGGGAGCATCAGCCTGAA 476
                                                    GTTCAAGAACGCCTACATGACGGACGTGGCCCCGGCTCCTGGCGAGCACCGGCGCGCCGCT 416
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(I (bases 1 to 854)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored BST resource
for barley genomics: Blumeria infected incompatible (Mla13)
seedling leaf cDNA library
On Nov 17, 2000 this sequence version replaced gi:11192753.
                                                                                                            939 CCCCGAGATCATGCAGGCCGGCGGCTGGACCAACGTGAACATCGTGATGAACTACATCCG
  GAGCGGCCACACACCGCCCCGCGCGCCCCCCCCGCGACATGGCCCCGCGCCGCGTGAGCAT
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/organism="Hordeum vulgare subsp. vulgare"
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Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence stop: 7
Location/Qualifiers
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Total hq bases = 509
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http://www.gernome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofe A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 304 c 249 g 149 t lothers
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                        Query Match 7.0%; Score 73.4; DB 29; Length 676; Best Local Similarity 48.8%; Pred. No. 0.0013; Matches 262; Conservative 0; Mismatches 266; Indels 9
                                                                                                                                                          /organism="Pseudomonas aeruginosa"
Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
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ORIGIN
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